



Query Match 54.5%; Score 911.4; DB 2; Length 1124;  
Best Local Similarity 96.5%; Pred. No. 1.2e-169;  
Matches 954; Conservative 0; Mismatches 6; Indels 29; Gaps 1;

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QY 1 GCAGCGGCGAGGCGCGGTGTGTGCTGAGTCCGTGTGTGCGAGAGGCGGAGGCGACAGCTC 60
DB 7 GCAGCGGCGAGGCGCGGTGTGTGCTGAGTCCGTGTGTGCGAGAGGCGGAGGCGACAGCTC 66
QY 61 -----ATCGGGTCCGGATAGGGCTGACGCTGCTCC 91
DB 67 TAGGGGTGGCAACCGCCCGAGAGAGGATCGGGGTCCGATAGGGCTGACGCTGCTCC 126
QY 92 TGTGTGCGGTGTGTGCTGAGCTTGACCTCGGCGCTCCGATAGAGAGGCGAGCGAGATG 151
DB 127 TGTGTGCGGTGTGTGCTGAGCTTGACCTCGGCGCTCCGATAGAGAGGCGAGCGAGATG 186
QY 152 AATCTTAGATTCCAAAGTACTTGTGACATGATGATGATGATGATGATGATGATGATGATG 211
DB 187 AATCTTAGATTCCAAAGTACTTGTGACATGATGATGATGATGATGATGATGATGATGATG 246
QY 212 CAGCGAGTACTTGTGTGTGATTTTCTTGATTTGAGAGATCTGATTAATGATCTT 271
DB 247 CAGCGAGTACTTGTGTGTGATTTTCTTGATTTGAGAGATCTGATTAATGATCTT 306
QY 272 CTATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 331
DB 307 CTATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 366
QY 332 TCAGCTTTCTAGAGTCTCCAAATCCAGAAACAAGAGCTATGAGAGAGAGAGAGAGAGTAC 391
DB 367 TCAGCTTTCTAGAGTCTCCAAATCCAGAAACAAGAGCTATGAGAGAGAGAGAGAGAGTAC 426
QY 392 GGAAGACAGCTTTGACCGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451
DB 427 GGAAGACAGCTTTGACCGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
QY 452 TTCTTTCTTAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 511
DB 487 TTCTTTCTTAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
QY 512 TGTGTGTGTCTACACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 571
DB 547 TGTGTGTGTCTACACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
QY 572 AAGAGAGAGCTGTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
DB 607 AAGAGAGAGCTGTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666
QY 632 TGAAGATCTTAATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691
DB 667 TGAAGATCTTAATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
QY 692 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
DB 727 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
QY 752 TGTGTGTGTCTGTGCAAGATATCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
DB 787 TGTGTGTGTCTGTGCAAGATATCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
QY 812 AGGAGAGAGCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 871
DB 847 AGGAGAGAGCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 906
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DB 907 TTAATTCAAGTCAAGCAAGAGCTCTTGATATATATATATATATATATATATATATATATAT 966
QY 932 TTAATGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 967 TTAATGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 995
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RESULT 2  
US-09-489-847-22  
; Sequence 22, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: P2031p1

; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 2876  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-489-847-22

Query Match 21.5%; Score 359.6; DB 4; Length 2876;  
Best Local Similarity 91.4%; Pred. No. 1.4e-61;  
Matches 404; Conservative 0; Mismatches 9; Indels 29; Gaps 1;

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QY 2 CAGCGGCGAGGCGCGGTGTGTGCTGAGTCCGTGTGTGCGAGAGGCGGAGCGACAGCTC 60
DB 10 CAGCGGCGAGGCGCGGTGTGTGCTGAGTCCGTGTGTGCGAGAGGCGGAGCGACAGCTC 69
QY 61 -----ATCGGGTCCGGATAGGGCTGACGCTGCTCC 92
DB 70 AGGGGTGGCAACCGCCCGAGAGAGAGATCGGGGTCCGATAGGGCTGACGCTGCTCC 129
QY 93 GGTGTGTGTGTGTGCTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG 152
DB 130 GGTGTGTGTGTGTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG 189
QY 153 ATCTTAGATTCCAAAGTACTTGTGACATGATGATGATGATGATGATGATGATGATGATG 212
DB 190 ATCTTAGATTCCAAAGTACTTGTGACATGATGATGATGATGATGATGATGATGATGATG 249
QY 213 AGGAGAGTACTTGTGTGCAATATTTCTTGATTCAGAGAGATCTGATTAATGATCTTC 272
DB 250 AGGAGAGTACTTGTGTGCAATATTTCTTGATTCAGAGAGATCTGATTAATGATCTTC 309
QY 273 TATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 332
DB 310 TATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 369
QY 333 CAGCTTTCTAGAGTCTCCAAATCCAGAAACAAGAGCTATGAGAGAGAGAGAGAGAGATG 392
DB 370 CAGCTTTCTAGAGTCTCCAAATCCAGAAACAAGAGCTATGAGAGAGAGAGAGAGATG 429
QY 393 GAAACAGCTTTGACCGGCAAT 414
DB 430 GAAACAGCTTTGCTGAGCAAT 451
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RESULT 3  
US-09-489-847-111  
; Sequence 111, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al